

SEQUENCE LISTING

(1) GENERAL INFORMATION:

- 5 (i) APPLICANT: Baker, Joffre
Chien, Kenneth
King, Kathleen
Pennica, Diane
Wood, William
- 10 (ii) TITLE OF INVENTION: Cardiac Hypertrophy Factor and Uses
Therefor
- 15 (iii) NUMBER OF SEQUENCES: 8
- (iv) CORRESPONDENCE ADDRESS:
(A) ADDRESSEE: Genentech, Inc.
(B) STREET: 460 Point San Bruno Blvd
(C) CITY: South San Francisco
20 (D) STATE: California
(E) COUNTRY: USA
(F) ZIP: 94080
- 25 (v) COMPUTER READABLE FORM:
(A) MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk
(B) COMPUTER: IBM PC compatible
(C) OPERATING SYSTEM: PC-DOS/MS-DOS
(D) SOFTWARE: patin (Genentech)
- 30 (vi) CURRENT APPLICATION DATA:
(A) APPLICATION NUMBER:
(B) FILING DATE: 05-AUG-1994
(C) CLASSIFICATION:
- 35 (vii) PRIOR APPLICATION DATA:
(A) APPLICATION NUMBER: 08/233609
(B) FILING DATE: 25-APR-1994
- 40 (viii) ATTORNEY/AGENT INFORMATION:
(A) NAME: Hasak, Janet E.
(B) REGISTRATION NUMBER: 28,616
(C) REFERENCE/DOCKET NUMBER: 894P1
- 45 (ix) TELECOMMUNICATION INFORMATION:
(A) TELEPHONE: 415/225-1896
(B) TELEFAX: 415/952-9881
(C) TELEX: 910/371-7168
- 50 (2) INFORMATION FOR SEQ ID NO:1:
- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1352 bases
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single

TCTTTTTGTT TCCTTGTCTC TTGGTTCTTT CTTTGCTTGC TTGCTTGCTT 900

5 GCTTGCTTGT TGTTGAGACA GGGTCTCACC ATATAGCTCT GGATGGCCTG 950

GAACTTGCTA TGTAGGCCAG GCTGGCCTCC AGCTCATAGA GATCCACTTG 1000

10 CCTCCGACTC CCAATTTCCC CATCTGTCTC CCTGTGATCC ATATGGGTAT 1050

GTGTAACCCT TACTTTGTCT CATGGAGGTG ACAATTTTTC TCCCTTCAGT 1100

15 TTCTTTGTTC TTTACTGACC AGAAAAGTGC CTACTTGTCC CCTGGTGGCA 1150

AGGCCATTCA CCTTAGGACC TTCCCACCAG TTCCTTTGTA GGCAAATCCC 1200

TCCCCCTTTG AGGTCCTTCC CTTTCATACC GCCCTAGGCT GGTCAATGGA 1250

25 GAGAGAAAGG CAGAAAAACA TCTTTAAAGA GTTTTATTTG AGAATAAATT 1300

AATTTTTGTA AATAAAATGT TTAACAATAA AACTAAACTT TTATGAAAAA 1350

30 AA 1352

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1352 bases
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

CCTATTCGGA CCCC GGTCGT ACTCGGTCTC CCTCCCTTCA GACCTTCTGG 50

50 TGGTCTGACT GAGGAGTTAG AGTAAGGATG GGGTAAACCT CCGGTTCTAG 100

GCGGTCTGTG TGTTGGAACG GGCGGAGGAC TGGTTTATAC GTCTTGTTGA 150

CACATTGGGA ATGAAACAGA GTACCTCCAC TGTAAAAAG AGGGAAGTCA 1100

AAGAAACAAG AAATGACTGG TCTTTTCACG GATGAACAGG GGACCACCGT 1150

TCCGGTAAGT GGAATCCTGG AAGGGTGGTC AAGGAAACAT CCGTTTAGGG 1200

AGGGGGAAAC TCCAGGAAGG GAAAGTATGG CGGGATCCGA CCAGTTACCT 1250

CTCTCTTTCC GTCTTTTGT AGAAATTCT CAAAATAAAC TCTTATTTAA 1300

TTAAAAACAT TTATTTTACA AATTGTTATT TTGATTTGAA AATACTTTTT 1350

TT 1352

(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 203 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

Met	Ser	Gln	Arg	Glu	Gly	Ser	Leu	Glu	Asp	His	Gln	Thr	Asp	Ser	1	5	10	15
Ser	Ile	Ser	Phe	Leu	Pro	His	Leu	Glu	Ala	Lys	Ile	Arg	Gln	Thr	20	25	30	
His	Asn	Leu	Ala	Arg	Leu	Leu	Thr	Lys	Tyr	Ala	Glu	Gln	Leu	Leu	35	40	45	
Glu	Glu	Tyr	Val	Gln	Gln	Gln	Gly	Glu	Pro	Phe	Gly	Leu	Pro	Gly	50	55	60	
Phe	Ser	Pro	Pro	Arg	Leu	Pro	Leu	Ala	Gly	Leu	Ser	Gly	Pro	Ala	65	70	75	
Pro	Ser	His	Ala	Gly	Leu	Pro	Val	Ser	Glu	Arg	Leu	Arg	Gln	Asp	80	85	90	
Ala	Ala	Ala	Leu	Ser	Val	Leu	Pro	Ala	Leu	Leu	Asp	Ala	Val	Arg	95	100	105	
Arg	Arg	Gln	Ala	Glu	Leu	Asn	Pro	Arg	Ala	Pro	Arg	Leu	Leu	Arg	110	115	120	

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	Ser	Leu	Glu	Asp	Ala	Ala	Arg	Gln	Val	Arg	Ala	Leu	Gly	Ala	Ala	125	130	135
5	Val	Glu	Thr	Val	Leu	Ala	Ala	Leu	Gly	Ala	Ala	Ala	Arg	Gly	Pro	140	145	150
	Gly	Pro	Glu	Pro	Val	Thr	Val	Ala	Thr	Leu	Phe	Thr	Ala	Asn	Ser	155	160	165
10	Thr	Ala	Gly	Ile	Phe	Ser	Ala	Lys	Val	Leu	Gly	Phe	His	Val	Cys	170	175	180
	Gly	Leu	Tyr	Gly	Glu	Trp	Val	Ser	Arg	Thr	Glu	Gly	Asp	Leu	Gly	185	190	195
15	Gln	Leu	Val	Pro	Gly	Gly	Val	Ala								200	203	

(2) INFORMATION FOR SEQ ID NO:4:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 200 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

	Met	Ala	Phe	Thr	Glu	His	Ser	Pro	Leu	Thr	Pro	His	Arg	Arg	Asp	1	5	10	15
30	Leu	Cys	Ser	Arg	Ser	Ile	Trp	Leu	Ala	Arg	Lys	Ile	Arg	Ser	Asp	20	25	30	
35	Leu	Thr	Ala	Leu	Thr	Glu	Ser	Tyr	Val	Lys	His	Gln	Gly	Leu	Asn	35	40	45	
	Lys	Asn	Ile	Asn	Leu	Asp	Ser	Ala	Asp	Gly	Met	Pro	Val	Ala	Ser	50	55	60	
40	Thr	Asp	Gln	Trp	Ser	Glu	Leu	Thr	Glu	Ala	Glu	Arg	Leu	Gln	Glu	65	70	75	
	Asn	Leu	Gln	Ala	Tyr	Arg	Thr	Phe	His	Val	Leu	Leu	Ala	Arg	Leu	80	85	90	
45	Leu	Glu	Asp	Gln	Gln	Val	His	Phe	Thr	Pro	Thr	Glu	Gly	Asp	Phe	95	100	105	
	His	Gln	Ala	Ile	His	Thr	Leu	Leu	Leu	Gln	Val	Ala	Ala	Phe	Ala	110	115	120	
50	Tyr	Gln	Ile	Glu	Glu	Leu	Met	Ile	Leu	Leu	Glu	Tyr	Lys	Ile	Pro	125	130	135	

Arg Asn Glu Ala Asp Gly Met Pro Ile Asn Val Gly Asp Gly Gly
140 145 150

Leu Phe Glu Lys Lys Leu Trp Gly Leu Lys Val Leu Gln Glu Leu
155 160 165

Ser Gln Trp Thr Val Arg Ser Ile His Asp Leu Arg Phe Ile Ser
170 175 180

Ser His Gln Thr Gly Ile Pro Ala Arg Gly Ser His Tyr Ile Ala
185 190 195

Asn Asn Lys Lys Met
200

(2) INFORMATION FOR SEQ ID NO:5:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 50 bases
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

GCGGCCGCGA GCTCGAATTC TTTTTTTTTT TTTTTTTTTT TTTTTTTTTT 50

(2) INFORMATION FOR SEQ ID NO:6:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1018 bases
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

GTGAAGGGAG CCGGGATCAG CCAGGGGCCA GCATGAGCCG GAGGGAGGGA 50

AGTCTGGAAG ACCCCCAGAC TGATTCCTCA GTCTCACTTC TTCCCCACTT 100

GGAGGCCAAG ATCCGTCAGA CACACAGCCT TGCGCACCTC CTCACCAAAT 150

ACGCTGAGCA GCTGCTCCAG GAATATGTGC AGCTCCAGGG AGACCCCTTC 200

GGGCTGCCCA GCTTCTCGCC GCCGCGGCTG CCGGTGGCCG GCCTGAGCGC 250

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CCCGGCTCCG AGCCACGCGG GGCTGCCAGT GCACGAGCGG CTGCGGCTGG 300
5  ACGCGGCGGC GCTGGCCGCG CTGCCCCCGC TGCTGGACGC AGTGTGTCGC 350
   CGCCAGGCCG AGCTGAACCC GCGCGCGCCG CGCCTGCTGC GCCGCCTGGA 400
10 GGACGCGGCG CGCCAGGCCC GGGCCCTGGG CGCCGCCGTG GAGGCCTTGC 450
   TGGCCGCGCT GGGCGCCGCC AACCGCGGGC CCCGGGCCGA GGGGGCCGCC 500
15 GCCACCGCCT CAGCCGCCTC CGCCACCGGG GTCTTCCCCG CCAAGGTGCT 550
   GGGGCTCCGC GTTTGCGGCC TCTACCGCGA GTGGCTGAGC CGCACCGAGG 600
20 GCGACCTGGG CCAGCTGCTG CCCGGGGGCT CGGCCTGAGC GCCGCGGGGC 650
   AGCTCGCCCC GCCTCCTCCC GCTGGGTTCG GTCTCTCCTT CCGCTTCTTT 700
25 GTCTTTCTCT GCCGCTGTCG GTGTCTGTCT GTCTGCTCTT AGCTGTCTCC 750
   ATTGCCTCGG CCTTCTTTGC TTTTGTGGG GGAGAGGGGA GGGGACGGGC 800
30 AGGGTCTCTG TCGCCCAGGC TGGGGTGCAG TGGCGCGATC CCAGCACTGC 850
   AGCCTCAACC TCCTGGGCTC AAGCCATCCT TCCGCCTCAG CTTCCCCAGC 900
40 AGCTGGGACT ACAGGCACGC GCCACCACAG CCGGCTAATT TTTTATTAA 950
   TTTTTGTAG AGACGAGGTT TCGCCATGTT GCCCAGGCTG GTCTTGAAC 1000
45 CCGGGGCTCA AGCGATCC 1018

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(2) INFORMATION FOR SEQ ID NO:7:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1018 bases

(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

5 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

CACTTCCCTC GGCCCTAGTC GGTCCCCGGT CGTACTCGGC CTCCCTCCCT 50
10 TCAGACCTTC TGGGGGTCTG ACTAAGGAGT CAGAGTGAAG AAGGGGTGAA 100
15 CCTCCGGTTC TAGGCAGTCT GTGTGTCGGA ACGCGTGGAG GAGTGGTTTA 150
TGC GACTCGT CGACGAGGTC CTTATACACG TCGAGGTCCC TCTGGGGAAG 200
20 CCCGACGGGT CGAAGAGCGG CGGCGCCGAC GGCCACCGGC CGGACTCGCG 250
GGGCCGAGGC TCGGTGCGCC CCGACGGTCA CGTGCTCGCC GACGCCGACC 300
25 TGC GCCCGCCG CGACCGGCGC GACGGGGGCG ACGACCTGCG TCACACAGCG 350
GCGGTCCGGC TCGACTTGGG CGCGCGCGGC GCGGACGACG CGGCGGACCT 400
30 CCTGCGCCGC GCGGTCCGGG CCCGGGACCC GCGGCGGCAC CTCCGGAACG 450
35 ACCGGCGCGA CCCGCGGCGG TTGGCGCCCG GGGCCCGGCT CGGGGGGCGG 500
CGGTGGCGGA GTCGGCGGAG GCGGTGGCCC CAGAAGGGGC GGTTCACGA 550
40 CCCCAGGGCG CAAACGCCGG AGATGGCGCT CACCGACTCG GCGTGGCTCC 600
CGCTGGACCC GGTCGACGAC GGGCCCCCGA GCCGGACTCG CGGCGCCCCG 650
45 TCGAGCGGGG CGGAGGAGGG CGACCCAAGG CAGAGAGGAA GGCGAAGAAA 700
50 CAGAAAGAGA CGGCGACAGC CACAGACAGA CAGACGAGAA TCGACAGAGG 750
TAACGGAGCC GGAAGAAACG AAAAACACCC CCTCTCCCCT CCCCTGCCCC 800

TCCCAGAGAC AGCGGGTCCG ACCCCACGTC ACCGCGCTAG GGTCGTGACG 850

TCGGAGTTGG AGGACCCGAG TTCGGTAGGA AGGCGGAGTC GAAGGGGTCG 900

TCGACCCTGA TGTCCGTGCG CGGTGGTGTC GGCCGATTAA AAAATAAATT 950

AAAAAACATC TCTGCTCCAA AGCGGTACAA CGGGTCCGAC CAGAACTTGA 1000

GGCCCCGAGT TCGCTAGG 1018

(2) INFORMATION FOR SEQ ID NO:8:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 201 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

Met	Ser	Arg	Arg	Glu	Gly	Ser	Leu	Glu	Asp	Pro	Gln	Thr	Asp	Ser
1				5				10						15
Ser	Val	Ser	Leu	Leu	Pro	His	Leu	Glu	Ala	Lys	Ile	Arg	Gln	Thr
			20					25						30
His	Ser	Leu	Ala	His	Leu	Leu	Thr	Lys	Tyr	Ala	Glu	Gln	Leu	Leu
			35					40						45
Gln	Glu	Tyr	Val	Gln	Leu	Gln	Gly	Asp	Pro	Phe	Gly	Leu	Pro	Ser
			50					55						60
Phe	Ser	Pro	Pro	Arg	Leu	Pro	Val	Ala	Gly	Leu	Ser	Ala	Pro	Ala
			65					70						75
Pro	Ser	His	Ala	Gly	Leu	Pro	Val	His	Glu	Arg	Leu	Arg	Leu	Asp
			80					85						90
Ala	Ala	Ala	Leu	Ala	Ala	Leu	Pro	Pro	Leu	Leu	Asp	Ala	Val	Cys
			95					100						105
Arg	Arg	Gln	Ala	Glu	Leu	Asn	Pro	Arg	Ala	Pro	Arg	Leu	Leu	Arg
			110					115						120
Arg	Leu	Glu	Asp	Ala	Ala	Arg	Gln	Ala	Arg	Ala	Leu	Gly	Ala	Ala
			125					130						135
Val	Glu	Ala	Leu	Leu	Ala	Ala	Leu	Gly	Ala	Ala	Asn	Arg	Gly	Pro
			140					145						150

